GGCTTCTCGTGGTTCCCAGAGCCCTGCTTAATGGATGGAGACTGGACGAGAACCTGGCTGCTGTGGTTCT GAACATGGCCCAGAGCCCTGTGTCTGCCGAGGTCATTCACCAGGTGGAAGAGTGTCTTGATGAAGACGAG AAGGAGATGATGCTCTTCCTGTGTAGAGATGTGACTGAGAACCTGGCTGCACCTAACGTCAGGGACCTCC ${\tt CACCTGGTTTCTGATTATAGGGTCCTGCTGATGGAGATTGGTGAGAGCTTAGATCAGAACGATGTATCCT}$ CCTTAGTTTTCCTTACAAGGATTACAAGGGATTACACAGGCAGAGGCAAGATAGCCAAGGACAAGAGTTT $\tt CTTGGATCTGGTGATTGAATTGGAGAAACTGAATCTAATTGCTTCAGACCAATTGAATTTGTTAGAAAAA$ TGCCTGAAGAACATCCACAGAATAGACTTGAACACAAAGATCCAGAAGTACACCCAGTCCAGCCAAGGAG TAGGAATCTGCTTGATCATTGATTGTATTGGCAACGACACAAAATATCTTCAAGAGACCTTCACTTCCCT GGGCTATCATATCCAGCTTTTCTTGTTTCCCAAGTCACATGACATAACCCAGATTGTTCGCCGATATGCA AGTATGGCCCAACATCAAGACTATGACAGCTTTGCATGTGTTCTGGTGAGCCTAGGAGGCTCCCAAAGCA TGATGGGCAGAGATCAAGTTCACTCAGGGTTCTCCTTGGATCATGTCAAGAACATGTTCACGGGGGACAC GAAGATAGCAGCCTGGAGGTAGATGGGCCATCAATAAAAAATGTGGACTCTAAGCCCCTGCAACCCAGAC ${\tt ACTGCACAACTCACCCAGAAGCTGATATCTTTTGGAGCCTGTGCACAGCAGACGTATCTCACTTGGAGAA}$ AATACAGCCTCAGCCTGCAGCACCTCTGAGGAAGAACTCATCCTGGCTCCTACGTGAGAACCCCAGAC GCCTGGGAAACGTCTCACTCCCGCCGCCGTGCCTTTACCTCTCTAAACTTCCCTACTTACATTCCTTAGT GGTTATCTACCAAGTTATACCAAGTTATTGTATGGGTGTATAGTGTATAGTGGTTCAAGATTCTGAATGT AACTTGAGACTTACCTGAGTTTGTCATGCGACTGGGTAAATTGTTTCTATGGCACATCTAATCATTTAAT AAGTAATTACCTCATTAAGTACCCATTGCTTCAGGACTTTCACATTGGCCACCAATTTCTGTGACCCAGC TCCACATTTATATTCTCTTTCGGCAAAACCAAATTTCATTATGTCTGTTTAATATCTACAGTCTAATGCT ${\tt TGCAGTGGCTTCGGTGAAAGGAGAATGAGCCCTACTCCTTGAAAGGTTGTAGTGCTTGGGAGAGCAGTCT}$ TTGGCTCAGGATCAGGAAACAGGAGGGATGACCAACTTGGGGCTTTGAGGTGGCCCACCCCAGCATCCAT ATCATCTGTGAACTGCCAGAGCCTGTGAAGGGGCGGGTCCTGTAGAACTAAGGCTGCAGGATCTCCATGA ${\tt CACAGGGCAACAACAGGGTATCTGAGAAGGGTCCCCGTGAGGGTCCAGTATTTATAGTGCACCAGAAGCC}$ AGAGGCCTCGGATCAGACAATGACCCATTGCACTGAGTAAAGATGTAAGTGAATGAGTGAAGATGTGTGG TGTTTCTTTGGCAGGAACAGATTGCAAGGGCAGAGAGTAGATAAGGAAGCTGGAGACATGAGTGGGGTTG

MAQSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAELLYRVRRFDLLKRILKTDKATVED HLRRNPHLVSDYRVLLMEIGESLDQNDVSSLVFLTRITRDYTGRGKIAKDKSFLDLVIELEKLNLIASDQLNLLEKCLKNIHRIDL NTKIQKYTQSSQGARSNMNTLQASLPKLSIKYNSRLQNGRSKEPRFVEYRDSQRTLVKTSIQESGAFLPPHIREETYRMQSKPLGI CLIIDCIGNDTKYLQETFTSLGYHIQLFLFPKSHDITQIVRRYASMAQHQDYDSFACVLVSLGGSQSMMGRDQVHSGFSLDHVKNM FTGDTCPSLRGKPKLFFIQNYESLGSQLEDSSLEVDGPSIKNVDSKPLQPRHCTTHPEADIFWSLCTADVSHLEKPSSSSSVYLQK LSQQLKQGRRRPLVDLHVELMDKVYAWNSGVSSKEKYSLSLQHTLRKKLILAPT (SEQ ID NO:2)

FIGURE 1

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

[GGCTTCTCGTGGTTCCCAGAGCCCTGCTTAATGGATGGAGACTGGACGAGAACCTGGCTG CTGTGGTTCTGAACATGGCCCAGAG] CCCTGTGTCTGCCGAGGTCATTCACCAGGTGGAAG <u>AGTGTCTTGATGAAGACGAGAAGGAGATGATGCTCTTCCTGTGTAGAGATGTGACTGAGA</u> **ACCTGGCTGCACCTAACGTCAGGGACCTCCTGGATAGCTTAAGTGAGAGAGGCCAGCTCT** CTTTGCTAC [CTTGGCTGAATTGCTCTACAGAGTGAGGCGGTTTGACCTTCTCAAGAGGA TCTTGAAGACAGACAAAGCAACCGTGGAGGACCACCTGCGCAGAAACCCTCACCTGGTTT ${\tt CTGATTATAG} \ {\tt [GGTCCTGCTGATGGAGATTGGTGAGAGCTTAGATCAGAACGATGTATCCT]}$ ${\tt CCTTAGTTTTCCTTACAAGGATTACAAGGGATTACACAGGCAGAGGCAAGATAGCCAAGG}$ ACAAGAGTTTCTTGGATCTGGTGATTGAATTGGAGAAACTGAATCTAATTGCTTCAGACC AATTGAATTTGTTAGAAAAATGCCTGAAGAACATCCACAGAATAGACTTGAACACAAAGA TCCAGAAGTACACCCAGTCCAGCCAAGGAGCAAGATCAAATATGAATACTCTCCAGGCTT CGCTCCCAAAATTGAGTATCAAGTATAACTCAAGGCTCCAGAATGGGCGAAGTAAAGAGC CAGGAGCTTTTTTACCTCCGCACATCCGTGAAGAGACTTACAGGATGCAGAGCAAGCCCC TAGGAATCTGCTTGATCATTGATTGTATTGGCAACGACACAAAATATCTTCAAGAGACCT TCACTTCCCTGGGCTATCATATCCAGCTTTTCTTGTTTCCCAAGTCACATGACATAACCC AGATTGTTCGCCGATATGCAAGTATGGCCCAACATCAAGACTATGACAGCTTTGCATGTG TTCTGGTGAGCCTAGGAGGCTCCCAAAGCATGATGGGCAGAGATCAAGTTCACTCAGGGT TCTCCTTGGATCATGTCAAGAACATGTTCACGGGGGACACGTGCCCTTCTCTCAGAGGGA AGCCAAAGCTCTTTTTTTTTCAGAACTATGAGTCGTTAGGTAGCCAGTTGGAAGATAGCA GCCTGGAGGTAGATGGGCCATCAATAAAAAATGTGGACTCTAAGCCCCTGCAACCCAGAC ACTGCACAACTCACCCAGAAGCTGATATCTTTTGGAGCCTGTGCACAGCAGACGTATCTC ACTTGGAGAAGCCCTCCAGCTCATCCTCTGTGTATCTGCAGAAGCTCTCCCAGCAGCTGA AGCAAGGCAGGAGACGCCCACTCGTGGACCTCCACGTTGAACTCATGGACAAAGTGTATG CGTGGAACAGTGGTGTTTCGTCTAAGGAGAAATACAGCCTCAGCCTGCAGCACACTCTGA GGAAGAAACTCATCCTGGCTCCTACGTGAGAACCCCAGACCGTTGGTGTTCTTGGTATAT GCTCTGCCGTGAGTCCTGGCCTAGGGTTCTCCTGTGCACAGGCATGAGCCGTAACCCTGT GCCTGGGAAACGTCTCACTCCCGCCGCCGTGCCTTTACCTCTCTAAACTTCCCTACTTAC ATTCCTTAGTCGGATGTTTTGCCAGAGTGTGGAGAACAGTAAGACATAAACCTATTGTTT ${\tt GTTTGTTTTTGGGGGGGGGGGTTATCTACCAAGTTATACCAAGTTATTGTATGGGTGTACCAAGTTATTGTATTGTATTGGGTGTACCAAGTTATTGTATTGTATTGGGTGTACAAGTTATTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATTGTATTGGGTGTATACCAAGTTATTGTATGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATGTATTGTATTGTATGTATTGTATTGTATTGTATGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTG$ TAGTGTATAGTGGTTCAAGATTCTGAATGTAACTTGAGACTTACCTGAGTTTGTCATGCG ACTGGGTAAATTGTTTCTATGGCACATCTAATCATTTAATAAGTAATTACCTCATTAAGT ACCCATTGCTTCAGGACTTTCACATTGGCCACCAATTTCTGTGACCCAGCTCCACATTTA TATTCTCTTTCGGCAAAACCAAATTTCATTATGTCTGTTTAATATCTACAGTCTAATGCT TTGTAAGACATCTAGATAGGAAAAATAGTTACCCATGAGCACAGGAGGGCTGGCCTGACC $\tt CTCACCAGCTGTGCAGTGGCTTCGGTGAAAGGAGAATGAGCCCTACTCCTTGAAAGGTTG$ ACACAACAGTGAGTGGGGGAGCTTGCCCTGGTTGGCTCAGGATCAGGAAACAGGAGGGAT GACCAACTTGGGGCTTTGAGGTGGCCCACCCCAGCATCCATATCATCTGTGAACTGCCAG ACAACAGGGTATCTGAGAAGGGTCCCCGTGAGGGTCCAGTATTTATAGTGCACCAGAAGC CAGAGGCCTCGGATCAGACAATGACCCATTGCACTGAGTAAAGATGTAAGTGAATGAGTG TTTGTTTGTTTGTTTTTTTTTTTTTTGCAGGAACAGATTGCAAGGGCAGAGAGTA GATAAGGAAGCTGGAGACATGAGTGGGGTTGGGTGCATGATATAGAATTCACAAAGAAAA AAAAAAAAA

Gene Sequence Structure *

86 bp

Sequence Deleted

250 bp

Size of full-length cDNA: 2770 bp

Targeting Vector* (genomic sequence)

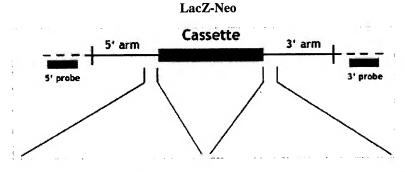
Construct Number: 3547

Arm Length: 5': 0.3 kb

3': 4.8 kb

Targeting Vector
Endogenous Locus

* Not drawn to scale



5'>CCTGTGCTTTGACTCTCAAGC CTAAGTGTTTTGATAAGAGGATTC TCTTTCACCACAGAGTGTCTCTAT TGCAAGAACTCTGAGAGAAATGAA GAGAGTCCTCAGCAATGATGTTGG CTTCTCGTGGTTCCCAGAGCCCTG CTTAATGGATGGAGACTGGACGAG AACCTGGCTGCTGTGGTTCTGAAC ATGGCCCAGAG<3'(SEQ ID NO:3) 5'>CTTGGCTGAATTGCTCTACAG AGTGAGGCGGTTTGACCTTCTCAA GAGGATCTTGAAGACAGACAAAGC AACCGTGGAGGACCACCTGCGCAG AAACCCTCACCTGGTTTCTGATTA TAGGTAAGTCATCCCCTGGGGAG GGGAGAGGGAGTCTAGATGGTTAG GGCAGTGAGAAGACCCCATTGCTT CCTCTTCTCTC<3'(SEQ ID NO:4)

Hot Plate

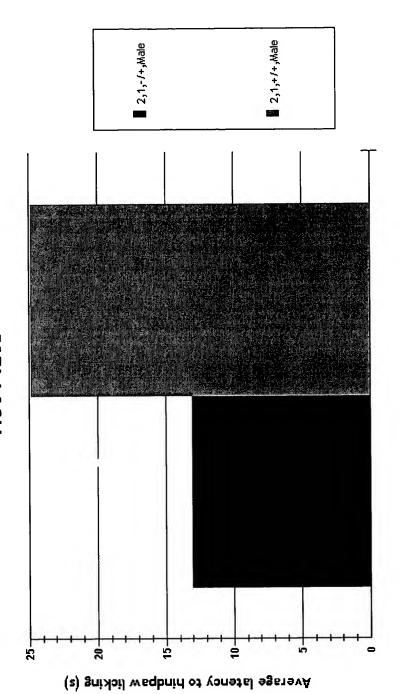


FIGURE 3

Metrazol

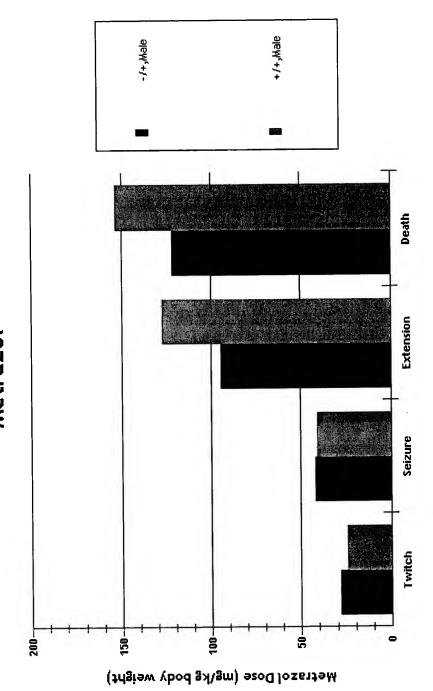


FIGURE 4